the AMPKG3F3/AMPKG3R2 PCR product. After an initial incubation at 95°C for 5 min, the following thermocycling profile was repeated 10 times: denaturation at 95°C (30 sec), and probe annealing and ligation at 55°C (90 sec). After OLA cycling, 1 μl of product was heat denatured at 94°C (3 min), cooled on ice, and loaded onto 6% polyacrylamide denaturing gel for electrophoresis on an ABI377 DNA sequencer (PERKIN ELMER, Foster City, USA). The resulting fragment lengths and peak fluorescence were analyzed using GENESCAN software (PERKIN ELMER, Foster City, USA). --

Replace the paragraph beginning at page 32, line 5, with the following rewritten paragraph:

-- A microsatellite 127B1 (*MS127B1*) was cloned from BAC 127G7 containing pig *PRKAG3*. The BAC clone was digested with *Sau*3AI and the restriction fragments subcloned into the *Bam*HI site of pUC18. The resulting library was probed with a $(CA)_{15}$ oligonucleotide probe labeled with [γ-32P]-dATP. Strongly hybridizing clones were sequenced and primers for PCR amplification of microsatellite loci were designed. Ten μl PCR reactions were performed containing 100 ng genomic DNA, 0.2 mM dNTPs, 1.5 mM $MgCl_2$, 4.0 pmol of both forward (MS127B1F:5' -Fluorescein-CAAACTCTTCTAGGCGTGT-3') (SEQ ID NO:38) and reverse (MS127B1R:5' -GTTTCTGGAACTTCCATATGCCATGG-3') (SEQ ID NO:39) primers, and 1 U of *Taq* DNA polymerase and reaction buffer (ADVANCED BIOTECH, London, UK). The cycling conditions included an initial incubation at 94°C for 5 min followed by 3 cycles at 94°C (1 min), 57°C (1 min) and 72°C (1 min), and 35 cycles of 94°C (20 sec), 55°C (30 sec) and 72°C (30 sec). The PCR products (0.3 μl) were separated using 4% polyacrylamide denaturing gel electrophoresis on an ABI377 DNA sequencer (PERKIN ELMER, Foster City, USA). The resulting fragment lengths were analyzed using the GENESCAN and GENOTYPER software (PERKIN ELMER, Foster City, USA). --

Replace the paragraph beginning at page 33, line 13, with the following rewritten paragraph:

-- Sequence of primers used to amplify the *RN* mutation region:

RNU: 5' GGGAACGATTCACCCTCAAC 3' (SEQ ID NO:40)

RNL: 5' AGCCCCTCCTCACCCACGAA 3' (SEQ ID NO:41) --

Replace the paragraph beginning at page 33, line 24, with the following rewritten paragraph:

-- The sequence of the RNL modified primer including a control tail with a *Bsr*BI site is:

RNLBsrA14: 5' $A_5C_2A_7$CCGCTCAGCCCCTCCTCACCCACGAA 3' (SEQ ID NO:42) --

Please replace the sequence listing with the substitute sequence listing.